



#8/5
4-20-01

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/424,028

Source: 165b

Date Processed by STIC: 3/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED
MAR 29 2001
TECH CENTER 1600/2901

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/424028

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 J _____ Use of <220>Feature (NEW RULES) Sequence(s) 1,4-19 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1656

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001
TIME: 14:53:37

Does Not Comply
Corrected Diskette Needed

Input Set : A:\ES.txt
Output Set: N:\CRF3\03212001\I424028.raw

see pgs 1-4

3 <110> APPLICANT: John Bridgham, Michael C. Pallas, Sydney Brenner, Kevin Corcoran, George
4 Golda

5 <120> TITLE OF INVENTION: Planar Arrays of Microparticle-Bound Polynucleotides

6 <130> FILE REFERENCE: 815

7 <140> CURRENT APPLICATION NUMBER: US 09/424,028

8 <141> CURRENT FILING DATE: 1999-11-16

9 <150> PRIOR APPLICATION NUMBER: US 08/862,610

10 <151> PRIOR FILING DATE: 1997-05-23

11 <160> NUMBER OF SEQ ID: 19

12 <170> SOFTWARE: Microsoft Word97

14 <210> SEQ ID NO: 1

15 <211> LENGTH: 78

16 <212> TYPE: DNA

17 <213> ORGANISM: Artificial Sequence

see item 12 on Envr Summary Sheet

18 <220> FEATURE:

19 <221> NAME/KEY: any of a, c, g, t, or u at indicated position

20 <222> LOCATION: 26-57

21 <223> OTHER INFORMATION: a, c, g, t, or u

22 <400> SEQUENCE: 1

23 actaatcgtc tcactattta attaaannnnnn nnnnnnnnnnn

24 nnnnnnnnnnn nnnnnnnnggt tttttttttt tttttttv

27 <210> SEQ ID NO: 2

28 <211> LENGTH: 17

29 <212> TYPE: DNA

30 <213> ORGANISM: Artificial Sequence

31 <220> FEATURE:

32 <223> OTHER INFORMATION: Adaptor.

33 <400> SEQUENCE: 2

34 ataggggtct tcggtac

37 <210> SEQ ID NO: 3

38 <211> LENGTH: 19

39 <212> TYPE: DNA

40 <213> ORGANISM: Artificial Sequence

41 <220> FEATURE:

42 <223> OTHER INFORMATION: Adaptor.

43 <400> SEQUENCE: 3

44 gatcagctgc tgcaaattt

46 <210> SEQ ID NO: 4

47 <211> LENGTH: 30

48 <212> TYPE: DNA

49 <213> ORGANISM: Artificial Sequence

see item 12 on Envr Summary Sheet

50 <220> FEATURE:

51 <221> NAME/KEY: any of a, c, g, t, or u at indicated position

52 <222> LOCATION: 2-4

53 <223> OTHER INFORMATION: a, c, g, t, or u

54 <400> SEQUENCE: 4

55 annntacagc tgcattccctt ggcgctgagg

*do not put this response
on <2217> line; it
goes on <2237> line;
<2217> responses
are found in
WIPO STANDARD ST.25,
Appendix 2, Tables
5 and 6*

*do not put this response
on <2217> line*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001
TIME: 14:53:38

Input Set : A:\ES.txt
Output Set: N:\CRF3\03212001\I424028.raw

58 <210> SEQ ID NO: 5
59 <211> LENGTH: 30
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence *item 12*
W--> 62 <220> FEATURE:
W--> 63 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
64 <222> LOCATION: 1, 3-4
65 <223> OTHER INFORMATION: a, c, g, t, or u
OK 66 <400> SEQUENCE: 5
67 nanntacagc tgcattccctg ggcctgtaag 30
68 <210> SEQ ID NO: 6
69 <211> LENGTH: 30
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence *item 12*
W--> 72 <220> FEATURE:
W--> 73 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
74 <222> LOCATION: 2-4
75 <223> OTHER INFORMATION: a, c, g, t, or u
OK 76 <400> SEQUENCE: 6
OK 77 cnnntacagc tgcattccctt gacgggtctc 30
78 <210> SEQ ID NO: 7
79 <211> LENGTH: 30
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence *item 12*
W--> 82 <220> FEATURE:
W--> 83 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
84 <222> LOCATION: 1, 3-4
85 <223> OTHER INFORMATION: a, c, g, t, or u
OK 86 <400> SEQUENCE: 7
OK 87 ncnnntacagc tgcattccctg cccgcacagt 30
88 <210> SEQ ID NO: 8
89 <211> LENGTH: 30
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence *item 12*
W--> 92 <220> FEATURE:
W--> 93 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
94 <222> LOCATION: 2-4
95 <223> OTHER INFORMATION: a, c, g, t, or u
OK 96 <400> SEQUENCE: 8
OK 97 gnnntacagc tgcattccctt cgctcgagac 30
98 <210> SEQ ID NO: 9
99 <211> LENGTH: 30
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence *item 12*
W--> 102 <220> FEATURE:
W--> 103 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
104 <222> LOCATION: 1, 3-4
105 <223> OTHER INFORMATION: a, c, g, t, or u
OK 106 <400> SEQUENCE: 9

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001
 TIME: 14:53:38

Input Set : A:\ES.txt
 Output Set: N:\CRF3\03212001\I424028.raw

OK 111 ngnttacagc tgcattccctg atccgctagc 30
 113 <210> SEQ ID NO: 10
 114 <211> LENGTH: 30
 115 <212> TYPE: DNA
 116 <213> ORGANISM: Artificial Sequence *Item 12*
 W--> 117 <220> FEATURE:
 W--> 118 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
 119 <222> LOCATION: 2-4
 120 <223> OTHER INFORMATION: a, c, g, t, or u
 OK 121 <400> SEQUENCE: 10 30
 122 tnnntacagc tgcattccctt ccgaacccgc
 124 <210> SEQ ID NO: 11
 125 <211> LENGTH: 30
 126 <212> TYPE: DNA
 127 <213> ORGANISM: Artificial Sequence *Item 12*
 W--> 128 <220> FEATURE:
 W--> 129 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
 130 <222> LOCATION: 1, 3-4
 131 <223> OTHER INFORMATION: a, c, g, t, or u
 OK 132 <400> SEQUENCE: 11 30
 133 ntnttacagc tgcattccctg agggggatag
 135 <210> SEQ ID NO: 12
 136 <211> LENGTH: 30
 137 <212> TYPE: DNA
 138 <213> ORGANISM: Artificial Sequence *Item 12*
 W--> 139 <220> FEATURE:
 W--> 140 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
 141 <222> LOCATION: 1-2, 4
 142 <223> OTHER INFORMATION: a, c, g, t, or u
 OK 143 <400> SEQUENCE: 12 30
 144 nnantacagc tgcattccctt cccgctacac
 146 <210> SEQ ID NO: 13
 147 <211> LENGTH: 30
 148 <212> TYPE: DNA
 149 <213> ORGANISM: Artificial Sequence *Item 12*
 W--> 150 <220> FEATURE:
 W--> 151 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
 152 <222> LOCATION: 1-3
 153 <223> OTHER INFORMATION: a, c, g, t, or u
 OK 154 <400> SEQUENCE: 13 30
 155 nnnatacagc tgcattccctg actccccgag
 157 <210> SEQ ID NO: 14
 158 <211> LENGTH: 30
 159 <212> TYPE: DNA
 160 <213> ORGANISM: Artificial Sequence *Item 12*
 W--> 161 <220> FEATURE:
 W--> 162 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
 163 <222> LOCATION: 1-2, 4
 164 <223> OTHER INFORMATION: a, c, g, t, or u

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001
TIME: 14:53:38

Input Set : A:\ES.txt
Output Set: N:\CRF3\03212001\I424028.raw

OK 165 <400> SEQUENCE: 14
W--> 166 nncntacagc tgcattccctg tgttgccgagg 30
168 <210> SEQ ID NO: 15
169 <211> LENGTH: 30
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence *Item 12*
W--> 172 <220> FEATURE:
W--> 173 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
174 <222> LOCATION: 1-3
175 <223> OTHER INFORMATION: a, c, g, t, or u
OK 176 <400> SEQUENCE: 15
W--> 177 nnnctacagc tgcattccctc tacagcagcg 30
179 <210> SEQ ID NO: 16
180 <211> LENGTH: 30
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence *Item 12*
W--> 183 <220> FEATURE:
W--> 184 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
185 <222> LOCATION: 1-2, 4
186 <223> OTHER INFORMATION: a, c, g, t, or u
OK 187 <400> SEQUENCE: 16
W--> 188 nngntacagc tgcattccctg tcgcgtcggtt 30
190 <210> SEQ ID NO: 17
191 <211> LENGTH: 30
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence *Item 12*
W--> 194 <220> FEATURE:
W--> 195 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
196 <222> LOCATION: 1-3
197 <223> OTHER INFORMATION: a, c, g, t, or u
OK 198 <400> SEQUENCE: 17
W--> 199 nnngtacagc tgcattccctc ggagcaacct 30
201 <210> SEQ ID NO: 18
202 <211> LENGTH: 30
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence *Item 12*
W--> 205 <220> FEATURE:
W--> 206 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
207 <222> LOCATION: 1,2,4
208 <223> OTHER INFORMATION: a, c, g, t, or u
W--> 209 <400> SEQUENCE: 18
W--> 210 nntntacagc tgcattccctg gtgaccgtag 30
212 <210> SEQ ID NO: 19
213 <211> LENGTH: 30
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence *Item 12*
W--> 216 <220> FEATURE:
W--> 217 <221> NAME/KEY: any of a, c, g, t, or u at indicated position
218 <222> LOCATION: 1-3

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001
TIME: 14:53:38

Input Set : A:\ES.txt
Output Set: N:\CRF3\03212001\I424028.raw

219 <223> OTHER INFORMATION: a, c, g, t, or u
OK-> 220 <400> SEQUENCE: 19
OK-> 221 nnnttacagc tgcattccctc ccctgtcgga

30

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001
TIME: 14:53:39

Input Set : A:\ES.txt
Output Set: N:\CRF3\03212001\I424028.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:283 W: Missing Blank Line separator, <140> field identifier
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:18 M:283 W: Missing Blank Line separator, <220> field identifier
L:19 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:22 M:283 W: Missing Blank Line separator, <400> field identifier
L:23 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:24 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:31 M:283 W: Missing Blank Line separator, <220> field identifier
L:33 M:283 W: Missing Blank Line separator, <400> field identifier
L:41 M:283 W: Missing Blank Line separator, <220> field identifier
L:43 M:283 W: Missing Blank Line separator, <400> field identifier
L:50 M:283 W: Missing Blank Line separator, <220> field identifier
L:51 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:54 M:283 W: Missing Blank Line separator, <400> field identifier
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:62 M:283 W: Missing Blank Line separator, <220> field identifier
L:63 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:66 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:73 M:283 W: Missing Blank Line separator, <220> field identifier
L:74 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:77 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:84 M:283 W: Missing Blank Line separator, <220> field identifier
L:85 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:88 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:95 M:283 W: Missing Blank Line separator, <220> field identifier
L:96 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:99 M:283 W: Missing Blank Line separator, <400> field identifier
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:106 M:283 W: Missing Blank Line separator, <220> field identifier
L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:110 M:283 W: Missing Blank Line separator, <400> field identifier
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:117 M:283 W: Missing Blank Line separator, <220> field identifier
L:118 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:121 M:283 W: Missing Blank Line separator, <400> field identifier
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:128 M:283 W: Missing Blank Line separator, <220> field identifier
L:129 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:132 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:139 M:283 W: Missing Blank Line separator, <220> field identifier
L:140 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:143 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001
TIME: 14:53:39

Input Set : A:\ES.txt
Output Set: N:\CRF3\03212001\I424028.raw

L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:150 M:283 W: Missing Blank Line separator, <220> field identifier
L:151 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:154 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:161 M:283 W: Missing Blank Line separator, <220> field identifier
L:162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:165 M:283 W: Missing Blank Line separator, <400> field identifier
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:172 M:283 W: Missing Blank Line separator, <220> field identifier
L:173 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:176 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:183 M:283 W: Missing Blank Line separator, <220> field identifier
L:184 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:187 M:283 W: Missing Blank Line separator, <400> field identifier
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:194 M:283 W: Missing Blank Line separator, <220> field identifier
L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:198 M:283 W: Missing Blank Line separator, <400> field identifier
L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:205 M:283 W: Missing Blank Line separator, <220> field identifier
L:206 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:209 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:216 M:283 W: Missing Blank Line separator, <220> field identifier
L:217 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:220 M:283 W: Missing Blank Line separator, <400> field identifier
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19